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OM nucleic - nucleic search, using sw model

Run on: March 11, 2004, 05:34:19 ; Search time 9440 Seconds
(without alignments)
11588.752 Million cell updates/sec

Title: US-09-989-734-A-351
Perfect score: 2524
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

RESULT 1

AX697283

LOCUS AX697283 2524 bp DNA linear PAT 02-APR-2003

DEFINITION Sequence 351 from Patent WO0078961.

ACCESSION AX697283

VERSION AX697283.1 GI:29498434

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ferrara,N., Stewart,T.A., Williams,P.M., Baker,K.P., Desnoyers,L.,
Eaton,D.L., Gao,W.Q., Pan,J., Botstein,D., Fong,S., Goddard,A.,
Godowski,P.J., Gurney,A.L., Smith,V., Tumas,D., Wood,W.I.,
Grimaldi,C.J., Hillan,K.J., Paoni,N.F., Roy,M.A. and Watanabe,C.K.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0078961-A 351 28-DEC-2000;
Genentech Inc. (US)

FEATURES Location/Qualifiers

source 1. .2524
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;

Matches 2524; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AY358534

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VERSION	AY358534.1 GI:37182190				
KEYWORDS	FLI_CDNA.				

SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 2524)
 AUTHORS Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
 Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
 Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
 Heldens,S., Huang,A., Kim,H.S., Klimowski,L., Jin,Y., Johnson,S.,
 Lee,J., Lewis,L., Liao,D., Mark,M., Robbie,E., Sanchez,C.,
 Schoenfeld,J., Seshagiri,S., Simmons,L., Singh,J., Smith,V.,
 Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
 Xie,M.H., Yansura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
 Goddard,A., Wood,W.I. and Godowski,P.

TITLE The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
 Effort to Identify Novel Human Secreted and Transmembrane Proteins:
 A Bioinformatics Assessment

JOURNAL Genome Res. 13 (10), 2265-2270 (2003)
 PUBMED 12975309

REFERENCE 2 (bases 1 to 2524)
 AUTHORS Clark,H.F.
 TITLE Direct Submission
 JOURNAL Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
 Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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ORIGIN

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Db	1381	CTCCTGGCTCCTGCCCCCTTGACACCACCCGGAACACTCCCCAGCCCCACGGGCAATCCT	1440
Qy	1441	ATCTGCTCGCCCTCCTGCAGGTGGGGGCCTCACATATCTGTGACTTCGGGTCCCTGTCCC	1500
Db	1441	ATCTGCTCGCCCTCCTGCAGGTGGGGGCCTCACATATCTGTGACTTCGGGTCCCTGTCCC	1500
Qy	1501	CACCCCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCACAGGCCATTTG	1560
Db	1501	CACCCCTTGTGCACTCACATGAAAGCCTTGACACTCACCTCCACCTTCACAGGCCATTTG	1560
Qy	1561	CACACGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGTGACTCTCATGTTCT	1620
Db	1561	CACACGCTCCTGCACCCTCTCCCCGTCCATACCGCTCCGCTCAGTGACTCTCATGTTCT	1620
Qy	1621	CTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAGTGGTCA	1680
Db	1621	CTCGTCTCACATTTGCACTCTCTCCTTCCCACATTCTGTGCTCAGCTCACTCAGTGGTCA	1680
Qy	1681	GCGTTTCCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGGTGTG	1740
Db	1681	GCGTTTCCTGCACACTTTACCTCTCATGTGCGTTTCCCGGCCTGATGTTGTGGTGGTGTG	1740
Qy	1741	CGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGCGT	1800
Db	1741	CGGCGTGCTCACTCTCTCCCTCATGAACACCCACCCACCTCGTTTCCGCAGCCCCCTGCGT	1800

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 11:46:45 ; Search time 108 Seconds
(without alignments)
6361.382 Million cell updates/sec

Title: US-09-989-734-356
Perfect score: 1238
Sequence: 1 gcgacgggcaggacgccccg.....caaaaaaaaaaaaaaaaaaaaaa 1238

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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6: /cgn2_6/ptodata/2/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%									
Result		Query									
No.	Score	Match	Length	DB	ID	Description					
1	71.4	5.8	82	4	US-09-833-381-83	Sequence 83, Appl					
2	68	5.5	5102	1	US-08-494-168-1	Sequence 1, Appli					
3	66.8	5.4	579	4	US-09-404-879A-273	Sequence 273, App					
4	66.8	5.4	579	4	US-09-338-933-273	Sequence 273, App					
5	66.8	5.4	579	4	US-09-215-681-273	Sequence 273, App					
6	66.8	5.4	579	4	US-09-216-003A-273	Sequence 273, App					
7	65.8	5.3	1868	1	US-08-392-367B-1	Sequence 1, Appli					
8	65.8	5.3	1868	3	US-08-893-467A-1	Sequence 1, Appli					
c 9	65.6	5.3	330	4	US-09-404-879A-274	Sequence 274, App					
c 10	65.6	5.3	330	4	US-09-338-933-274	Sequence 274, App					
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	13	64.6	5.2	3120	4	US-09-169-768-29	Sequence 29, Appl
	14	63.8	5.2	444	4	US-09-397-787-161	Sequence 161, App
	15	63.6	5.1	1839	1	US-08-383-744-1	Sequence 1, Appli
	16	63.6	5.1	1839	2	US-08-999-336-1	Sequence 1, Appli
	17	63.6	5.1	1839	5	PCT-US96-01427-1	Sequence 1, Appli
c	18	63.6	5.1	7218	1	US-08-232-463-14	Sequence 14, Appl
	19	63	5.1	801	4	US-09-404-879A-216	Sequence 216, App
	20	63	5.1	801	4	US-09-338-933-216	Sequence 216, App
	21	63	5.1	801	4	US-09-215-681-216	Sequence 216, App
	22	63	5.1	801	4	US-09-216-003A-216	Sequence 216, App
	23	62.6	5.1	855	4	US-09-552-204A-10	Sequence 10, Appl
	24	62.6	5.1	1341	2	US-08-945-848-7	Sequence 7, Appli
	25	62.6	5.1	2363	2	US-08-945-848-6	Sequence 6, Appli
	26	62	5.0	3170	4	US-09-169-768-1	Sequence 1, Appli
	27	61.4	5.0	3171	4	US-09-169-768-15	Sequence 15, Appl
	28	61.4	5.0	3181	1	US-08-655-086-1	Sequence 1, Appli
	29	61.4	5.0	3349	4	US-09-169-768-13	Sequence 13, Appl
	30	61.4	5.0	3541	4	US-09-169-768-9	Sequence 9, Appli
	31	61.4	5.0	4409	4	US-09-331-347C-22	Sequence 22, Appl
	32	61.2	4.9	369	4	US-09-535-521-24	Sequence 24, Appl
c	33	61.2	4.9	369	4	US-09-535-521-26	Sequence 26, Appl
	34	61.2	4.9	384	4	US-09-535-521-7	Sequence 7, Appli
c	35	61.2	4.9	384	4	US-09-535-521-9	Sequence 9, Appli
	36	61.2	4.9	417	4	US-09-535-521-10	Sequence 10, Appl
c	37	61.2	4.9	417	4	US-09-535-521-12	Sequence 12, Appl
	38	61.2	4.9	423	4	US-09-535-521-13	Sequence 13, Appl
c	39	61.2	4.9	423	4	US-09-535-521-15	Sequence 15, Appl
	40	61.2	4.9	561	4	US-09-535-521-16	Sequence 16, Appl
c	41	61.2	4.9	561	4	US-09-535-521-18	Sequence 18, Appl
	42	61.2	4.9	624	4	US-09-535-521-19	Sequence 19, Appl
c	43	61.2	4.9	624	4	US-09-535-521-21	Sequence 21, Appl
	44	61.2	4.9	876	4	US-09-535-521-4	Sequence 4, Appli
c	45	61.2	4.9	876	4	US-09-535-521-6	Sequence 6, Appli

ALIGNMENTS

RESULT 1

US-09-833-381-83

; Sequence 83, Application US/09833381

; Patent No. 6672186

; GENERAL INFORMATION:

; APPLICANT: Robison, Keith E.

; TITLE OF INVENTION: No. 6672186el Nucleic Acid and Protein Homologs

; FILE REFERENCE: 5800-119

; CURRENT APPLICATION NUMBER: US/09/833,381

; CURRENT FILING DATE: 2001-04-11

; PRIOR APPLICATION NUMBER: 09/516,448

; PRIOR FILING DATE: 2000-02-29

; NUMBER OF SEQ ID NOS: 2050

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 83

; LENGTH: 82

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-833-381-83

Query Match 5.8%; Score 71.4; DB 4; Length 82;
Best Local Similarity 92.6%; Pred. No. 4.6e-09;
Matches 75; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 741 CAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGAT 800
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 Db 1 CAACAAGTGGCGCACGGGTGAGCCCAACAATGCCTACGACGAGGAGGACTGCGTGGAGAT 60
 Qy 801 GGTGGCCTCGGGCGGCTGGAA 821
 |||
 Db 61 GGTGGCCTCGGGAAAATGGAA 81

RESULT 2

US-08-494-168-1

; Sequence 1, Application US/08494168

; Patent No. 5731192

: GENERAL INFORMATION:

APPLICANT: Reeders, Stephen T.

APPLICANT: Zhou, Jing

5
; TITLE OF INVENTION: Collagen COL4A6: Gene, Protein and Method

TITLE OF INVENTION: of Detecting Collagen Deficiency

NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

ADDRESSEE: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
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; COMPUTER:  IBM PC compatible

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;      OPERATING SYSTEM:  PC-DOS/MS-DOS

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; SOFTWARE: PatentIn Release #1.0, Version #1.25
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CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/494,168

FILING DATE:

CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/112,465

FILING DATE: 27-AUG-1993

; ATTORNEY/AGENT INFORMATION:

NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 40397/104/BABR

; TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399

TELEX: 904136

; INFORMATION FOR SEQ ID NO: 1:

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; SEQUENCE CHARACTERISTICS:

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;      LENGTH:  5102 base pairs
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; TYPE: nucleic acid

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; STRANDEDNESS: double
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;      TOPOLOGY:  linear
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; FEATURE:
; NAME/KEY: CDS
; LOCATION: join(2..82, 86..97, 101..4399, 4403..4420, 4424
; LOCATION: ..4465, 4469..4876, 4880..5101)
US-08-494-168-1

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Query Match          5.5%; Score 68; DB 1; Length 5102;
Best Local Similarity 56.8%; Pred. No. 1.9e-07;
Matches 125; Conservative 0; Mismatches 95; Indels 0; Gaps 0;

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Qy      185 CTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCTGGAA 244
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Db      2913 CTGGACGCGCTGGTACTCCTGGTGAAAAGGGAGACAGAGGCAATCCGGGGCCAGTCGGAA 2972

Qy      245 GAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGTGTGG 304
          | | | | | | | | | | | | | | | | | | | | | | | | | |
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Qy      305 GTCGTCATGGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAAGGAGATTCCGGTGACA 364
          | | | | | | | | | | | | | | | | | | | | | | | | | |
Db      3033 GCTCAGCCGGATCCAATGGATTTCTGGGCCAAGAGGTGACAAAGGAGAGGCTGGTCGAC 3092

Qy      365 TAGGACCCCCTGGTCTTAATGGAGAACCAGGCCTCCCATG 404
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Db      3093 CTGGACCACCAGGCCTACCTGGAGCTCCTGGCCTCCAGG 3132

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RESULT 3

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US-09-404-879A-273
; Sequence 273, Application US/09404879A
; Patent No. 6468546
; GENERAL INFORMATION:
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF OVARIAN CANCER
; FILE REFERENCE: 210121.462C2
; CURRENT APPLICATION NUMBER: US/09/404,879A
; CURRENT FILING DATE: 1999-09-24
; NUMBER OF SEQ ID NOS: 393
; SOFTWARE: FastSEQ for Windows Version 3.0
; SEQ ID NO 273
; LENGTH: 579
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(579)
; OTHER INFORMATION: n = A,T,C or G
US-09-404-879A-273

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Query Match          5.4%; Score 66.8; DB 4; Length 579;
Best Local Similarity 52.0%; Pred. No. 1.5e-07;
Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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Qy      117 GTCACTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGAT 176

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Db      7  GTCGCGGCCGAGGTCTGGCCCTCCTGGCAAGGCTGGTGAAGATGGTCACCCCTGGAAAAACC 66

QY      177 CCTCGTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACG 236
      | |||| | ||| | || | ||| | |||| | || | ||| |||
Db      67  CGGACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCCTGGAAC 126

QY      237 GCCTGGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGG 296
      ||||| | ||| || || | ||| ||| || | ||| ||| ||
Db      127 TCCTGGACTTCCTGGCTTCAAAGGCATTAGGGGACACAATGGTCTGGATGGATTGAAGGG 186

QY      297 CAGTGTGGGTGCTCATGGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTC 356
      ||| || ||| | ||| ||| | |||| | ||| ||| ||
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QY      357 CGGTGACATAGGACCCCTGGTCCTAATGGAGAACCAGGCC 397
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RESULT 4

US-09-338-933-273

; Sequence 273, Application US/09338933

; Patent No. 6488931

; GENERAL INFORMATION:

; APPLICANT: Mitcham, Jennifer Lynn

; APPLICANT: King, Gordon E.

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY OF

; TITLE OF INVENTION: OVARIAN CANCER

; FILE REFERENCE: 210121.462C1

; CURRENT APPLICATION NUMBER: US/09/338,933

; CURRENT FILING DATE: 1999-06-23

; NUMBER OF SEQ ID NOS: 312

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 273

; LENGTH: 579

; TYPE: DNA

; ORGANISM: Homo sapien

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)...(579)

; OTHER INFORMATION: n = A,T,C or G

US-09-338-933-273

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Best Local Similarity 52.0%; Pred. No. 1.5e-07;

Matches 146; Conservative 0; Mismatches 135; Indels 0; Gaps 0;

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QY      177 CCTCGTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACG 236
      | |||| | ||| | || | ||| | |||| | || | ||| |||
Db      67  CGGACGACCTGGTGAGAGAGGAGTTGTTGGACCACAGGGTGCTCGTGGTTTCCCTGGAAC 126

QY      237 GCCTGGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGG 296

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 21, 2004, 11:45:05 ; Search time 5092 Seconds
(without alignments)
10537.839 Million cell updates/sec

Title: US-09-989-734-356
Perfect score: 1238
Sequence: 1 gcgacgggcaggacgccccg.....caaaaaaaaaaaaaaaaaaaaaa 1238

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

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Post-processing: Minimum Match 0%
Maximum Match 100%
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 32: em_htg_other:*
 33: em_htg_mus:*
 34: em_htg_pln:*
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 37: em_htg_vrt:*
 38: em_sy:*
 39: em_htgo_hum:*
 40: em_htgo_mus:*
 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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4	1238	100.0	1238	6	AX491060	AX491060 Sequence
5	1238	100.0	1238	9	AY358439	AY358439 Homo sapi
6	1226.8	99.1	1248	9	BC000078	BC000078 Homo sapi
7	1142.6	92.3	1417	9	BC009951	BC009951 Homo sapi
8	1132	91.4	1341	6	BD103302	BD103302 Novel col
9	978	79.0	1269	6	BD103330	BD103330 Novel col
10	978	79.0	1269	6	BD103331	BD103331 Novel col
11	950.6	76.8	1139	6	BD103303	BD103303 Novel col
12	877	70.8	1067	6	BD103305	BD103305 Novel col
13	834	67.4	1197	6	BD103329	BD103329 Novel col
14	832.2	67.2	1067	6	BD103306	BD103306 Novel col
15	813	65.7	813	6	BD103332	BD103332 Novel col
16	805.6	65.1	995	6	BD103304	BD103304 Novel col
17	733.4	59.2	139357	9	AC010907	AC010907 Homo sapi
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19	675.4	54.6	1522	6	BD103307	BD103307 Novel col
20	659	53.2	741	6	BD103340	BD103340 Novel col
21	659	53.2	741	6	BD103341	BD103341 Novel col
22	641.8	51.8	813	6	BD103338	BD103338 Novel col
23	613	49.5	663	6	BD103336	BD103336 Novel col
24	568.2	45.9	663	6	BD103337	BD103337 Novel col
25	545.2	44.0	669	6	BD103339	BD103339 Novel col
26	541.6	43.7	591	6	BD103335	BD103335 Novel col
27	477	38.5	477	6	BD103334	BD103334 Novel col
28	458.6	37.0	1272	5	BC056052	BC056052 Xenopus l
29	391.4	31.6	619	6	BD103308	BD103308 Novel col
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31	322.2	26.0	246539	2	AC125638	AC125638 Rattus no
32	251.6	20.3	867	10	AB016429	AB016429 Mus muscu
33	247.6	20.0	1016	6	AX376032	AX376032 Sequence

	34	247.6	20.0	1016	9	AY359038	AY359038 Homo sapi
	35	246	19.9	1594	9	AB002631	AB002631 Homo sapi
	36	246	19.9	1595	6	E29008	E29008 Novel colle
	37	226.4	18.3	212049	5	BX005484	BX005484 Zebrafish
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c	39	212.4	17.2	321	6	AX408538	AX408538 Sequence
	40	160.2	12.9	234922	2	AC097055	AC097055 Rattus no
	41	157	12.7	141262	9	AC080033	AC080033 Homo sapi
c	42	157	12.7	182475	2	AC023487	AC023487 Homo sapi
	43	154.8	12.5	166900	2	AC115924	AC115924 Mus muscu
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ALIGNMENTS

RESULT 1

AR252616

LOCUS AR252616 1238 bp DNA linear PAT 20-DEC-2002

DEFINITION Sequence 356 from patent US 6478825.

ACCESSION AR252616

VERSION AR252616.1 GI:27300524

KEYWORDS

SOURCE Unknown.

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1238)

AUTHORS Winterbottom,J.M., Shimp,L., Boyce,T.M. and Kaes,D.

TITLE Implant, method of making same and use of the implant for the treatment of bone defects

JOURNAL Patent: US 6478825-A 356 12-NOV-2002;

FEATURES Location/Qualifiers

source 1. .1238

/organism="unknown"

/mol_type="genomic DNA"

ORIGIN

Query Match 100.0%; Score 1238; DB 6; Length 1238;

Best Local Similarity 100.0%; Pred. No. 1.4e-210;

Matches 1238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db	1	GCGACGGGCAGGACGCCCCGTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTCTGCCTGCG	60
Qy	61	CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA	120
Db	61	CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA	120
Qy	121	CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC	180
Db	121	CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC	180
Qy	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCT	240
Db	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCT	240

Qy	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Db	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Qy	301	GTGGGTCGTCATGGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Db	301	GTGGGTCGTCATGGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Qy	361	GACATAGGACCCCCTGGTCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Db	361	GACATAGGACCCCCTGGTCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Qy	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Db	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Qy	481	ATCAAGAATGCTGTGCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Db	481	ATCAAGAATGCTGTGCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Qy	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Db	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Qy	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Db	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Qy	661	GCCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Db	661	GCCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Qy	721	CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Db	721	CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Qy	781	GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Db	781	GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Qy	841	ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Db	841	ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Qy	901	CCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC	960
Db	901	CCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC	960
Qy	961	CAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT	1020
Db	961	CAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT	1020
Qy	1021	AAACTGAGAAAATGGCCTATGCTTAAGAGGAAAAATGAAAGTGTTCTGGGGTGCTGTCTC	1080
Db	1021	AAACTGAGAAAATGGCCTATGCTTAAGAGGAAAAATGAAAGTGTTCTGGGGTGCTGTCTC	1080

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Qy      1081 TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140
          |||
Db      1081 TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140

Qy      1141 CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATAACAATAAAATCTTTAAG 1200
          |||
Db      1141 CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATAACAATAAAATCTTTAAG 1200

Qy      1201 TAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA 1238
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Db      1201 TAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAAA 1238

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RESULT 2

AX403469

LOCUS AX403469 1238 bp DNA linear PAT 14-JUN-2002

DEFINITION Sequence 356 from Patent WO0073454.

ACCESSION AX403469

VERSION AX403469.1 GI:21436970

KEYWORDS .

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Ashkenazi,A.J., Baker,K.P., Botstein,D., Desnoyers,L., Eaton,D.,
Ferrara,N., Gerber,H., Gerritsen,M., Goddard,A., Godowski,P.,
Grimaldi,C.J., Gurney,A.L., Kljavin,I., Napier,M.A., Pan,J.,
Paoni,N.F., Roy,M., Stewart,T.A., Tumas,D., Watanabe,C.K.,
Williams,P., Wood,W.I. and Zhang,Z.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same

JOURNAL Patent: WO 0073454-A 356 07-DEC-2000;
Genentech Inc. (US)

FEATURES

source

Location/Qualifiers

1. .1238

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1238; DB 6; Length 1238;

Best Local Similarity 100.0%; Pred. No. 1.4e-210;

Matches 1238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCGACGGGCAGGACGCCCCGTTTCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCG 60
          |||
Db      1 GCGACGGGCAGGACGCCCCGTTTCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCG 60

Qy      61 CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA 120
          |||
Db      61 CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA 120

Qy      121 CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC 180
          |||
Db      121 CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC 180

```

Qy	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCT	240
Db	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCCGGACGGCCT	240
Qy	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Db	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Qy	301	GTGGGTCGTCATGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Db	301	GTGGGTCGTCATGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Qy	361	GACATAGGACCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Db	361	GACATAGGACCCCTGGTCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Qy	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Db	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Qy	481	ATCAAGAATGCTGTGCGCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Db	481	ATCAAGAATGCTGTGCGCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Qy	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Db	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Qy	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Db	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Qy	661	GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Db	661	GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Qy	721	CACTCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Db	721	CACTCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Qy	781	GAGGAGGACTGCGTGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Db	781	GAGGAGGACTGCGTGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Qy	841	ACCATGTACTTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Db	841	ACCATGTACTTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Qy	901	CCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC	960
Db	901	CCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC	960
Qy	961	CAGCCAGGGAGCTGTCCCTCTGTGAAGGTTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT	1020
Db	961	CAGCCAGGGAGCTGTCCCTCTGTGAAGGTTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT	1020
Qy	1021	AAACTGAGAAAATGGCCTATGCTTAAGAGGAAAAATGAAAGTGTTCTGGGGTGCTGTCTC	1080

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Db      1021  |||||AAACTGAGAAAATGGCCTATGCTTAAGAGGAAAATGAAAGTGTTCTGCGGTGCTGTCTC 1080
Qy      1081  TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140
Db      1081  |||||TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140
Qy      1141  CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATACAATAAAATCTTTAAG 1200
Db      1141  |||||CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATACAATAAAATCTTTAAG 1200
Qy      1201  TAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA 1238
Db      1201  |||||TAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA 1238

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RESULT 3

AX454582

LOCUS AX454582 1238 bp DNA linear PAT 06-JUL-2002

DEFINITION Sequence 167 from Patent WO0208284.

ACCESSION AX454582

VERSION AX454582.1 GI:21713915

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker,K.P., Ferrara,N., Gerber,H., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Gurney,A.L., Hillan,K.J., Marsters,S.A., Pan,J.,
Paoni,N.F., Stephan,J.P., Watanabe,C.K., Williams,P.M., Wood,W.I.
and Ye,W.

TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis

JOURNAL Patent: WO 0208284-A 167 31-JAN-2002;
Genentech, Inc. (US) ; Baker, Kevin P. (US) ; Ferrara, Napoleone
(US) ; Gerber, Hanspeter (US) ; Gerritsen, Mary E. (US) ; Goddard,
Audrey (US) ; Godowski, Paul J. (US) ; Gurney, Austin L. (US) ;
Hillan, Kenneth J. (US) ; Marsters, Scot A. (US) ; Pan, James (US)
; Paoni, Nicholas F. (US) ; Stephan, Jean-Philippe F. (US) ;
Watanabe, Colin K. (US) ; Williams, P. Mickey (US) ; Wood, William
I. (US)

FEATURES

source Location/Qualifiers
1. .1238
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1238; DB 6; Length 1238;
Best Local Similarity 100.0%; Pred. No. 1.4e-210;
Matches 1238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCG 60
Db      1 GCGACGGGCAGGACGCCCCGTTTCGCCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCG 60

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Qy	61	CTCAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA	120
Db	61	CTCAGGATGAGGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA	120
Qy	121	CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC	180
Db	121	CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC	180
Qy	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCT	240
Db	181	GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCT	240
Qy	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Db	241	GGAAGAGTCGGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT	300
Qy	301	GTGGGTCGTCATGGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Db	301	GTGGGTCGTCATGGAAAAATTGGTCCCATTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT	360
Qy	361	GACATAGGACCCCCCTGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Db	361	GACATAGGACCCCCCTGGTCTTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG	420
Qy	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Db	421	CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC	480
Qy	481	ATCAAGAATGCTGTGCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Db	481	ATCAAGAATGCTGTGCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG	540
Qy	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCTCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Db	541	GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCTCTGCCAGGGCCGCGGGGGCACGCTGAGC	600
Qy	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Db	601	ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG	660
Qy	661	GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Db	661	GCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC	720
Qy	721	CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Db	721	CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC	780
Qy	781	GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Db	781	GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC	840
Qy	841	ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Db	841	ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC	900
Qy	901	CCATTGGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC	960

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Db      901 CCATTGGGGGCCCCACATGTCCCTGCAGGGTTGGCAGGGACAGAGCCCAGACCATGGTGC 960
Qy      961 CAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT 1020
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Db      961 CAGCCAGGGAGCTGTCCCTCTGTGAAGGGTGGAGGCTCACTGAGTAGAGGGCTGTTGTCT 1020
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      |||
Db      1021 AAAC TGAGAAAATGGCCTATGCTTAAGAGGAAAATGAAAGTGTTCCTGGGGTGCTGTCTC 1080
Qy      1081 TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140
      |||
Db      1081 TGAAGAAGCAGAGTTTCATTACCTGTATTGTAGCCCCAATGTCATTATGTAATTATTACC 1140
Qy      1141 CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATACAATAAAATCTTTAAG 1200
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Db      1141 CAGAATTGCTCTTCCATAAAGCTTGTGCCTTTGTCCAAGCTATACAATAAAATCTTTAAG 1200
Qy      1201 TAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA 1238
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Db      1201 TAGTGCAGTAGTTAAGTCCAAAAAAAAAAAAAAAAAAAA 1238

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RESULT 4

AX491060

LOCUS AX491060 1238 bp DNA linear PAT 16-AUG-2002

DEFINITION Sequence 167 from Patent WO0200690.

ACCESSION AX491060

VERSION AX491060.1 GI:22323867

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker, K.P., Ferrara, N., Gerber, H., Gerritsen, M.E., Goddard, A.,
Godowski, P.J., Gurney, A.L., Hillan, K.J., Marsters, S.A., Pan, J.,
Paoni, N.F., Stephan, J.P., Watanabe, C.K., Williams, P.M., Wood, W.I.
and Ye, W.

TITLE Compositions and methods for the diagnosis and treatment of
disorders involving angiogenesis

JOURNAL Patent: WO 0200690-A 167 03-JAN-2002;
Genentech, Inc. (US)

FEATURES

Location/Qualifiers

source

1. .1238
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 1238; DB 6; Length 1238;
Best Local Similarity 100.0%; Pred. No. 1.4e-210;
Matches 1238; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy      1 GCGACGGGCAGGACGCCCCGTTTCGCTAGCGCGTGCTCAGGAGTTGGTGTCTCCTGCCTGCG 60
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Db 1 GCGACGGGCAGGACGCCCCGTTGCGCTAGCGCGTGCTCAGGAGTTGGTGTCTGCCTGCG 60

Qy 61 CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA 120
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Db 61 CTCAGGATGAGGGGAATCTGGCCCTGGTGGGCGTTCTAATCAGCCTGGCCTTCCTGTCA 120

Qy 121 CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC 180
 |||

Db 121 CTGCTGCCATCTGGACATCCTCAGCCGGCTGGCGATGACGCCTGCTCTGTGCAGATCCTC 180

Qy 181 GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCT 240
 |||

Db 181 GTCCCTGGCCTCAAAGGGGATGCGGGAGAGAAGGGAGACAAAGGCGCCCCGGACGGCCT 240

Qy 241 GGAAGAGTCGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT 300
 |||

Db 241 GGAAGAGTCGCCCCACGGGAGAAAAAGGAGACATGGGGGACAAAGGACAGAAAGGCAGT 300

Qy 301 GTGGGTTCGTTCATGGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT 360
 |||

Db 301 GTGGGTTCGTTCATGGAAAAATTGGTCCCATTTGGCTCTAAAGGTGAGAAAGGAGATTCCGGT 360

Qy 361 GACATAGGACCCCCCTGGTCCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG 420
 |||

Db 361 GACATAGGACCCCCCTGGTCCCTAATGGAGAACCAGGCCTCCCATGTGAGTGCAGCCAGCTG 420

Qy 421 CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC 480
 |||

Db 421 CGCAAGGCCATCGGGGAGATGGACAACCAGGTCTCTCAGCTGACCAGCGAGCTCAAGTTC 480

Qy 481 ATCAAGAATGCTGTGCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG 540
 |||

Db 481 ATCAAGAATGCTGTGCGCCGGTGTGCGCGAGACGGAGAGCAAGATCTACCTGCTGGTGAAG 540

Qy 541 GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCCTGCCAGGGCCGCGGGGGCACGCTGAGC 600
 |||

Db 541 GAGGAGAAGCGCTACGCGGACGCCCAGCTGTCCTGCCAGGGCCGCGGGGGCACGCTGAGC 600

Qy 601 ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG 660
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Db 601 ATGCCCAAGGACGAGGCTGCCAATGGCCTGATGGCCGCATACCTGGCGCAAGCCGGCCTG 660

Qy 661 GCCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC 720
 |||

Db 661 GCCCCGTGTCTTCATCGGCATCAACGACCTGGAGAAGGAGGGCGCCTTCGTGTACTCTGAC 720

Qy 721 CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC 780
 |||

Db 721 CACTCCCCCATGCGGACCTTCAACAAGTGGCGCAGCGGTGAGCCCAACAATGCCTACGAC 780

Qy 781 GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC 840
 |||

Db 781 GAGGAGGACTGCGTGGAGATGGTGGCCTCGGGCGGCTGGAACGACGTGGCCTGCCACACC 840

Qy 841 ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC 900
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Db 841 ACCATGTACTTCATGTGTGAGTTTGACAAGGAGAACATGTGAGCCTCAGGCTGGGGCTGC 900